

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Zancope-Oliveia, Rosely M.
et al.,

(ii) TITLE OF INVENTION: Nucleic Acids of the M Antigen
Gene of Histoplasma Capsulatum, Isolated and
Recombinantly-Produced
Antigens, Vaccines and Antibodies, Method

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fitch, Even, Tabin & Flannery
(B) STREET: 135 South LaSalle Street, Suite 900
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60603-4277

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kaba, Richard A
(B) REGISTRATION NUMBER: 30,562
(C) REFERENCE/DOCKET NUMBER: 6314/62527

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-372-7842
(B) TELEFAX: 312-372-7848
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Histoplasma capsulatum
(B) STRAIN: var. capsulatum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCTGCT	GGCTCCGATA	ACTTTGCTTT	ATCCAAGGGT	CTCGGCGAAT	GCCAGGTGCC	60
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	GGTGTGGCCC	TTGATGCATA	TGGTTTATTT	ATAGCCGCCC	GGAAGCCCTG	GCCTGTAAAA	240
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	TCCCCATTIG	GGTTCCCTAT	AGGCCACTGC	GTGCTCCACT	CAAGAAGGGT	CCCAGTCAAT	360
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	ATTGATTATT	TGTCTTCTTC	AGCATCTTTT	TGTCTCGAGC	AAGCTTACTC	CACGTTCAAT	480
	TCAGGGGGTA	AAAATGCGGT	CGCTCAAGCT	TATACTCGCC	TCGGCGGGTG	TTGTTTCTGC	540
	AGCCTGTCCC	TACATGTCAG	GGGAGATGCC	TAGCGGTGAG	AAAGGCCCCC	TCGATCGCCG	600
	CCATGACACT	CTCTCCGACC	CTACGGACCA	GTTTCTTAGC	AAGTTTTACA	TTGACGATGA	660
10	ACAGTCGGTG	CTAACAACGG	ACGTGGGTGG	TCCCATCGAG	GACCAACACA	GCCTGAAGGC	720
	TGGAAATAGA	GGCCCCAATC	TACTTGAGGA	TTTTATCTTC	CGCCAGAAGA	TTCAACACTT	780
	TGATCATGAG	AGGGTATGTA	GATACAAAAT	ATGTGACCGT	GTTGCAAATC	CGCTAATTCA	840
	ATTTTACGCA	GGTTCCTGAG	CGCGCCGTCC	ATGCTCGAGG	AGCTGGTGCC	CATGGCGTAT	900
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	CTGCTCGCGA	TATCCACGGA	TTTGCGACCC	GTCTGTATAC	CGATGAAGGC	AATTTTGGTA	1080
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	TTCAGGACGC	TATTCAATTC	CCTGATTTGA	TTACGCTGT	CAAGCCGCAA	CCAGACAGTG	1260
20	AAATTTCCCA	GGCTGCAACT	GCACATGATA	CGGCATGGGA	TTTCCTCAGC	CAGCAGCCCA	1320
	GCTCATTTGCA	TGCCCTCTTC	TGGGCAATGT	CAGGACATGG	AATCCCTCGC	TCAATCGGTC	1380
	ATGTTGATGG	GTGGGGCGTC	CATACCTTCC	GACTTGTAC	CGACGAGGGC	AACTCGACCT	1440
	TGGTCAAGTT	TCGCTGGAAG	ACCCTCCAAG	GAAGAGCGGG	CCTGGTATGG	GAAGAGGCAC	1500
	AGGCTCTTGG	CGGAAAGAAT	CCCGACTTCC	ATCGACAAGA	CCTCTGGGGT	GCCATTGAAT	1560
25	CTGGAAGGTA	CCCTGAGTGG	GAGGTAAAGT	ATGATTTCCC	CAAATCATT	GTCTGACAG	1620
	TGTTTTCTCTG	CTCTGTGCGT	TGCTCTTTTC	GTCTTTTTCT	ATATCTTCAA	CTAAGACTGA	1680
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	CAAGTTTGAT	TTCGATCTAT	TAGTCCCAC	CAAAATCATC	CCAGAAGAAC	TTGTTCCCTT	1800
	CACCCCAATC	GGAAAAATGG	TCTTGAACCG	AAACCCAAAA	AGTTATTTTG	CCGAAACTGA	1860
30	GCAGATCATG	GTTGGTCCAC	CCCCTATATA	TTTGGAATAT	GAATACATGT	ATAGCTAGAT	1920
	GAAGCGTATA	TCTAAATATA	TTTCCACAGT	TCCAACCAGG	TCATGTAGTT	CGCGGAATCG	1980
	ATTTACCGGA	TGACCCTTTG	CTTCAGGGCC	GCTTGTACTC	CTACCTTGAC	ACTCAATTGA	2040
	ATCGCCATGG	AGGTCCCAAC	TTGAGCAAC	TGCCGATCAA	CAGACCCCGC	ATCCCATTCC	2100
35	ATAACAACAA	TCGCGACGGT	GCTGGTAAGC	TACTTCTCAC	CTACCATGTC	AACTTCCATC	2160
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	CCCTCTAAAC	ACGGCCGCAT	ATACACCCAA	CTCAATGAGC	AACGGATTCC	CACAACAAGC	2280
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	AGTGCGCGAG	CTCAGCCCGA	GCTTCAACGA	CGTCTGGTCC	CAACCGCGTC	TCTTCTACAA	2400
40	CTCACTCACG	GTCTTCGAGA	AGCAATTCCT	CGTCAACGCC	ATGCGCTTCG	AAAACCCCA	2460
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	CTACCAACAAC	AAGGCAACCG	TCCCATCGG	CACCTTCGGC	ACGAATCTCC	TGCGGCTCGA	2640
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	CTGTTTTTCC	ATCTTTGGTT	GAGGTAAAT	TGCAGATATC	AGTAAATTGC	GTTTACGAAA	3240
	GCCGGTGTCA	AGCTTCANGA	GGCCTAATTA	ATTTGAAGAG	GAGTTGAAG	TGAAATCTTG	3300
55	GTGTAACATC	AATAATTTAT	AATAACTAAT	AACTTATAAT	TAATGTCTAT	TGTAATTTCC	3360
	TCTCACATTC	AATCTATATT	TGATCCTTGT	CCTTTGTAGC	TGTTTAAATA	TAAGCCAAGA	3420
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	TCAGATATTA	TCTATCATGT	TGTAATGATA	CCTCAAAAAT	GCCACAAGCT	TGCCTGATAT	3540
	TGAATATTTA	TATGCTGTAA	ATGTAGGGAA	GAGCGTACCA	TCCAAATAAC	CAGAAAAACA	3600
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60	TGACTATCTG	ATAAAAATGT	CTGTATTCC	GCTTCACGAC	GCATGTTATG	ACTTTCGAAT	3720
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	ACAACACCTT	CAAAAAGGAT	CC				3862

(2) INFORMATION FOR SEQ ID NO:2:

- 65 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 707 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

1 Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu
 5 Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
 Gln Ser Val 20 Thr Thr Asp Val 25 Gly Gly Pro Ile Glu Asp Gln His
 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
 10 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
 15 Lys Gln Thr 100 Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
 20 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
 25 Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
 30 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
 35 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
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 Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
 Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
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 Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
 50 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
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 Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
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 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
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 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
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 580 585 590
 Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
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 610 615 620
 10 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
 625 630 635 640
 Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
 645 650 655
 15 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
 660 665 670
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 675 680 685
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 20 Ser Leu Val
 705

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30 Ser Asp Pro Thr Asp Gln Phe Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

50 Thr Leu Gln Gly Arg Ala Gly Leu Val
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Gly Arg Tyr Pro Glu
1 5

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
1 5 10

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ile Ile Pro Glu Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AARAYCCVG AYTTY

15

45 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

[illegible]

TTNCCDATNG TRAA

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGAATCCTC CGACCCTACG GA

22

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
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(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCAAGCTTC TATCCAACGG GAACCGA

27

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY
THE
DEPARTMENT OF HEALTH AND HUMAN SERVICES CENTERS FOR DISEASE
CONTROL AND

PREVENTION
ZANCOPE-OLIVEIRA, ROSALY M.
LOTT, TIMOTHY J.
MAYER, LEONARD W.
REISS, ERROL
DEEPE, JR., GEORGE S.

<120> NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
HISTOPLASMA CAPSULATUM, ISOLATED AND RECOMBINANTLY-PRODUCED
ANTIGENS, VACCINES AND ANTIBODIES, METHODS AND KITS FOR
DETECTING HISTOPLASMOSIS

<130> 65798 / US

<140> NYA

<141> 1999-04-27

<150> U.S. 60/083,676

<151> 1998-04-30

<150> PCT/US99/09151

<151> 1999-04-27

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3863

<212> DNA

<213> Histoplasma capsulatum

<400> 1

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ctgactatct	gataaaaatg	tctgtatttc	cgttccacga	cgcattgtat	gactttcgaa	3720
tatagataaa	acctgaacga	tttagccctt	gttgggggaa	ataggggtta	ggggggcgag	3780

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 <211> 705
 <212> PRT
 <213> Histoplasma capsulatum

<400> 2
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 20 25 30
 Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
 35 40 45
 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
 50 55 60
 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
 65 70 75 80
 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
 85 90 95
 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
 100 105 110
 Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
 115 120 125
 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
 130 135 140
 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
 145 150 155 160
 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
 165 170 175
 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
 180 185 190
 Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
 195 200 205
 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
 210 215 220
 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
 225 230 235 240
 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
 245 250 255
 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
 260 265 270
 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
 275 280 285
 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
 290 295 300
 Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
 305 310 315 320
 Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
 325 330 335
 Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val

340 345 350
 Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
 355 360 365
 Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
 370 375 380
 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
 385 390 395 400
 Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
 405 410 415
 Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
 420 425 430
 Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
 435 440 445
 Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
 450 455 460
 Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
 465 470 475 480
 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
 485 490 495
 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
 500 505 510
 Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
 515 520 525
 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
 530 535 540
 Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
 545 550 555 560
 Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
 565 570 575
 Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
 580 585 590
 Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
 595 600 605
 Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
 610 615 620
 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
 625 630 635 640
 Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
 645 650 655
 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
 660 665 670
 Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
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 Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
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 Ser
 705

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<212> PRT

<213> Histoplasma capsulatum

5

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1 5

<210> 4
<211> 15
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<213> Histoplasma capsulatum

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<211> 9
<212> PRT
<213> Histoplasma capsulatum

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Thr Leu Gln Gly Arg Ala Gly Leu Val
1 5

<210> 6
<211> 16
<212> PRT
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<400> 6
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1 5 10 15

<210> 7
<211> 6
<212> PRT
<213> Histoplasma capsulatum

<400> 7
Ser Gly Arg Tyr Pro Glu
1 5

<210> 8
<211> 10
<212> PRT
<213> Histoplasma capsulatum

<400> 8
Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
1 5 10

<210> 9
<211> 14
<212> PRT

<213> Histoplasma capsulatum

<400> 9

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1 5 10

<210> 10

<211> 15

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<213> Unknown

<220>

<223> Primer

<400> 10

aaraayccvg aytty

15

<210> 11

<211> 14

<212> DNA

<213> Unknown

<220>

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<400> 11

ttnccdatng traa

14

<210> 12

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Primer

<400> 12

cggaatcctc cgaccctacg ga

22

<210> 13

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Primer

<400> 13

accaagcttc tatccaacgg gaaccga

27